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3'UTR seed matches, but not overall identity, are associated with RNAi off-targets

A Birmingham, EM Anderson, A Reynolds, D Ilsley, ... - *Nature Methods*, 2006 - [nature.com](#)

... There is a Corrigendum (June 2007) associated with this **Article**. ... that contain matches with any given siRNA seed region is very large in comparison to the ...

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BLAT-The BLAST-Like Alignment Tool - [*genome.org](#) [HTML]

WJ Kent - *Genome Research*, 2002 - Cold Spring Harbor Lab

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[PDF] •Automated generation of heuristics for biological sequence comparison

GS Slater, E Birney - *BMC Bioinformatics*, 2005 - [biomedcentral.com](#)

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J Soding - *Bioinformatics*, 2005 - Oxford Univ Press

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[HTML] •Fast and sensitive multiple alignment of large genomic sequences

M Brudno, M Chapman, B Gottgens, S Batzoglou, B ... - *BMC Bioinformatics*, 2003 - [biomedcentral.com](#)

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N Bray, I Dubchak, L Pachter - *Genome Research*, 2003 - Cold Spring Harbor Lab

... running AVID and displaying alignments using VISTA is ... Article published online before print in December 2002. ... for large-scale genome alignment and comparison. ...

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AR Panchenko, SH Bryant - *Protein Science*, 2002 - [prosci.highwire.org](#)

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C Guda, S Lu, ED Scheeff, PE Bourne, IN Shindyalov - *Nucleic Acids Research*, 2004 - [pt.wkhealth.com](#)

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Z Zhang, AA Schaffer, W Miller, TL Madden, DJ ... - *Nucleic Acids Research* - Oxford Univ Press

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[HTML] • [ProSup: a refined tool for protein structure alignment](#)

P Lackner, WA Koppensteiner, MJ Sippl, FS ... - Protein Engineering Design and Selection, 2000 - Oxford Univ Press

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